FIG. 1A

```
1 ATGGAGTCGGGGCTGCTGCGGCCGGCGCCGGTGAGCGAGGTCATCGTCCTGCATTACAAC
  M  E  S  G  L  L  R  P  A  P  V  S  E  V  I  V  L  H  Y  N

61 TACACCGGCAAGCTCCGCGGTGCGCGCTACCAGCCGGGTGCCGGCCTGCGCGCCGACGCC
   Y  T  G  K  L  R  G  A  R  Y  Q  P  G  A  G  L  R  A  D  A

121 GTGGTGTGCCTGGCGGTGTGCGCCTTCATCGTGCTAGAGAATCTAGCCGTGTTGTTGGTG
    V  V  C  L  A  V  C  A  F  I  V  L  E  N  L  A  V  L  L  V

181 CTCGGACGCCACCCGCGCTTCCACGCTCCCATGTTCCTGCTCCTGGGCAGCCTCACGTTG
    L  G  R  H  P  R  F  H  A  P  M  F  L  L  L  G  S  L  T  L

241 TCGGATCTGCTGGCAGGCGCCGCCTACGCCGCCAACATCCTACTGTCGGGGCCGCTCACG
    S  D  L  L  A  G  A  A  Y  A  A  N  I  L  L  S  G  P  L  T

301 CTGAAACTGTCCCCCGCGCTCTGGTTCGCACGGGAGGGAGGCGTCTTCGTGGCACTCACT
    L  K  L  S  P  A  L  W  F  A  R  E  G  G  V  F  V  A  L  T

361 GCGTCCGTGCTGAGCCTCCTGGCCATCGCGCTGGAGCGCAGCCTCACCATGGCGCGCAGG
    A  S  V  L  S  L  L  A  I  A  L  E  R  S  L  T  M  A  R  R

421 GGGCCCGCGCCCGTCTCCAGTCGGGGGCGCACGCTGGCGATGGCAGCCGCGGCCTGGGGC
    G  P  A  P  V  S  S  R  G  R  T  L  A  M  A  A  A  A  W  G

481 GTGTCGCTGCTCCTCGGGCTCCTGCCAGCGCTGGGCTGGAATTGCCTGGGTCGCCTGGAC
    V  S  L  L  L  G  L  L  P  A  L  G  W  N  C  L  G  R  L  D

541 GCTTGCTCCACTGTCTTGCCGCTCTACGCCAAGGCCTACGTGCTCTTCTGCGTGCTCGCC
    A  C  S  T  V  L  P  L  Y  A  K  A  Y  V  L  F  C  V  L  A
```

FIG. 1B

601 TTCGTGGGCATCCTGGCCGCTATCTGTGCACTCTACGCGCGCATCTACTGCCAGGTACGC
F V G I L A A I C A L Y A R I Y C Q V R

661 GCCAACGCGCGGCGCCTGCCGGCACGGCCCGGGACTGCGGGGACCACCTCGACCCGGGCG
A N A R R L P A R P G T A G T T S T R A

721 CGTCGCAAGCCGCGCTCGCTGGCCTTGCTGCGCACGCTCAGCGTGGTGCTCCTGGCCTTT
R R K P R S L A L L R T L S V V L L A F

781 GTGGCATGTTGGGGCCCCCTCTTCCTGCTGCTGTTGCTCGACGTGGCGTGCCCGGCGCGC
V A C W G P L F L L L L L D V A C P A R

841 ACCTGTCCTGTACTCCTGCAGGCCGATCCCTTCCTGGGACTGGCCATGGCCAACTCACTT
T C P V L L Q A D P F L G L A M A N S L

901 CTGAACCCCATCATCTACACGCTCACCAACCGCGACCTGCGCCACGCGCTCCTGCGCCTG
L N P I I Y T L T N R D L R H A L L R L

961 GTCTGCTGCGGACGCCACTCCTGCGGCAGAGACCCGAGTGGCTCCCAGCAGTCGGCGAGC
V C C G R H S C G R D P S G S Q Q S A S

1021 GCGGCTGAGGCTTCCGGGGGCCTGCGCCGCTGCCTGCCCCCGGGCCTTGATGGGAGCTTC
A A E A S G G L R R C L P P G L D G S F

1081 AGCGGCTCGGAGCGCTCATCGCCCCAGCGCGACGGGCTGGACACCAGCGGCTCCACAGGC
S G S E R S S P Q R D G L D T S G S T G

1141 AGCCCCGGTGCACCCACAGCCGCCCGGACTCTGGTATCAGAACCGGCTGCAGACTGA
S P G A P T A A R T L V S E P A A D *

FIG. 2

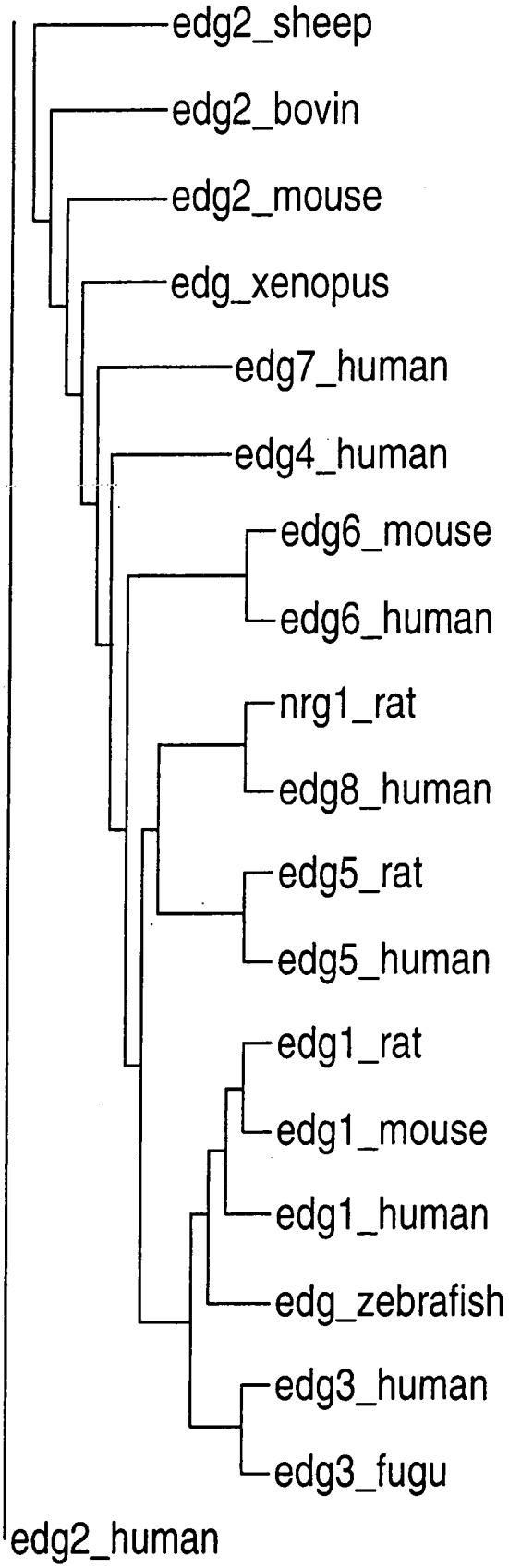


FIG. 3A

```
            1                                                          60
edg2_human  MAAISTSIPV ISQPQETAMN EPQCFYNESI AFFYNRSGKH LAT.EWNTVS KLVMGL..GI
edg7_human  ---------- --------MN E..CHYDKHM DFFYNRSNTD TVD.DW.TGT KLVIVLCVGT
edg4_human  ---------- -------MVI MGQCYYNETI GFFYNNSGKE LSS.HWR..P KDVVVVALGL
edg1_human  -----MGPTS VPLVKAHRSS VSDYVNYDII VRHYNYTGKL ..NISADKEN SIKLTSVVFI
edg3_human  ---------- --MATALPPR LQPVRGNETL REHYQYVGKL AGRLKEASEG S.TLTTVLFL
edg5_human  ---------- ------MGSL YSEYLNPNKV QEHYNYTKE. ..TLETQETT SRQVASAFIV
edg8_human  ---------- -----MESGL LRPAPVSEVI VLHYNYTGKL RG.ARYQPGA GLRADAVVCL
edg6_human  -----MNATG TPVAPESCQQ LAAGGHSRLI VLHYNHSGRL AGR.GGPEDG GLGALRGLSV

            61                                                        120
edg2_human  TVCIFIMLAN LLVMVAIYVN RRFHFPIYYL MANLAAADFF AGLAYFYLMF MTGPNTRRLT
edg7_human  FFCLFIFFSN SLVIAAVIKN RKFHFPFYYL LANLAAADFF AGIAYVFLMF NTGPVSKTLT
edg4_human  TVSVLVLLTN LLVIAAIASN RRFHQPIYYL LGNLAAADLF AGVAYLFLMF HTGPRTARLS
edg1_human  LICCFIILEN IFVLLTIWKT KKFHPPMYYF IGNLALSDLL AGVAYTANLL LSGATTYKLT
edg3_human  VICSFIVLEN LMVLIAIWKN NKFHNRMYFF IGNLALCDLL AGIAYKVNIL MSGKKTFSLS
edg5_human  ILCCAIVVEN LLVLIAVARN SKFHSAMYLF LGNLAASDLL AGVAFVANTL LSGSVTLRLT
edg8_human  AVCAFIVLEN LAVLLVLGRH PRFHAPMFLL LGSLTLSDLL AGAAYAANIL LSGPLTLKLS
edg6_human  AASCLVVLEN LLVLAAITSH MRSRRWVYYC LVNITLSDLL TGAAYLANVL LSGARTFRLA

            121                                                       180
edg2_human  VSTWLLRQGL IDTSLTASVA NLLAIAIERH ITVFR.MQLH TRMSNRRVVV VIVVIWTMAI
edg7_human  VNRWFLRQGL LDSSLTASLT NLLVIAVERH MSIMR.MRVH SNLTKKRVTL LILLVWAIAI
edg4_human  LEGWFLRQGL LDTSLTASVA TLLAIAVERH RSVMA.VQLH SRLPRGRVVM LIVGVWVAAI
edg1_human  PAQWFLREGS MFVALSASVF SLLAIAIERY ITMLK.MKLH NGSNNFRLFL LISACWVISL
edg3_human  PTVWFLREGS MFVALGASTC SLLAIAIERH LTMIK.MRPY DANKRHRVFL LIGMCWLIAF
edg5_human  PVQWFAREGS ASITLSASVF SLLAIAIERH VAIAK.VKLY GSDKSCRMLL LIGASWLISL
edg8_human  PALWFAREGG VFVALTASVL SLLAIALERS LTMAR.RGPA PVSSRGRTLA MAAAAWGVSL
edg6_human  PAQWFLREGL LFTALAASTF SLLFTAGERF ATMVRPVAES GATKTSPVYG FIGLCWLLAA

            181                                                       240
edg2_human  VMGAIPSVGW NCICDIENCS NMAPLYSDSY LVFWAIFNLV TFVVMVVLYA HIFGYVRQRT
edg7_human  FMGAVPTLGW NCLCNISACS SLAPIYSRSY LVFWTVSNLM AFLIMVVVYL RIYVYVKRKT
edg4_human  GLGLLPAHSW HCLCALDRCS RMAPLLSRSY LAVWALSSLL VFLLMVAVYT RIFFYVRRRV
edg1_human  ILGGLPIMGW NCISALSSCS TVLPLYHKHY ILFCTTVFTL LLLSIVILYC RIYSLVRTRS
edg3_human  TLGALPILGW NCLHNLPDCS TILPLYSKKY IAFCISIFTA ILVTIVILYA RIYFLVKSSS
edg5_human  VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI ILLAIVALYV RIYCVVRSSH
edg8_human  LLGLLPALGW NCLGRLDACS TVLPLYAKAY VLFCVLAFVG ILAAICALYA RIYCQVRANA
edg6_human  LLGMLPLLGW NCLCAFDRCS SLLPLYSKRY ILFCLVIFAG VLATIMGLYG AIFRLVQASG
```

FIG. 3B

```
             241                                                       300
edg2_human   MRMSRHSSGP R......RNR DTMMSLLKTV VIVLGAFIIC WTPGLVLLLL D.VCCP..QC
edg7_human   NVLSPHTSGS I......SRR RTPMKLMKTV MTVLGAFVVC WTPGLVVLLL DGLNCR..QC
edg4_human   QRMAEHVSCH P......RYR ETTLSLVKTV VIILGAFVVC WTPGQVVLLL DGLGCE..SC
edg1_human   RRLTFR.... .KNISKASRS SENVALLKTV IIVLSVFIAC WAPLFILLLL DV.GCKVKTC
edg3_human   RKVANH.... .NN......S ERSMALLRTV VIVVSVFIAC WSPLFILFLI DV.ACRVQAC
edg5_human   ADMA...... .........A PQTLALLKTV TIVLGVFIVC WLPAFSILLL DY.ACPVHSC
edg8_human   RRLPARPGTA GTTSTRARRK PRSLALLRTL SVVLLAFVAC WGPLFLLLLL DV.ACPARTC
edg6_human   QKAP...... ...RPAARRK ARR..LLKTV LMILLAFLVC WGPLFGLLLA DVFGSNLWAQ

             301                                                       360
edg2_human   DVLAYEKFFL LLAEFNSAMN PIIYSYRDKE MSATFRQILC CQRSENPTGP TESSDRSASS
edg7_human   GVQHVKRWFL LLALLNSVVN PIIYSYKDED MYGTMKKMIC CFSQENP... ....ERRPSR
edg4_human   NVLAVEKYFL LLAEANSLVN AAVYSCRDAE MRRTFRRLLC CACLRQSTRE SVHYTSSAQG
edg1_human   DILFRAEYFL VLAVLNSGTN PIIYTLTNKE MRRAFIRIMS CCKCPSGD.. .........S
edg3_human   PILFKAQWFI VLAVLNSAMN PVIYTLASKE MRRAFFRLV. .CNC.LVR.. .........G
edg5_human   PILYKAHYFF AVSTLNSLLN PVIYTWRSRD LRREVLRPLQ CWRPGVGV.. .........Q
edg8_human   PVLLQADPFL GLAMANSLLN PIIYTLTNRD LRHALLRLVC CGRHSCGRDP SGS..QQSAS
edg6_human   EYLRGMDWIL ALAVLNSAVN PIIYSFRSRE VCRAVLSFLC CGCLRLGMRG PGDCLARAVE

             361                                                  418
edg2_human   LNHTILAGVH SNDHSVV--- ---------- ---------- ---------- --------
edg7_human   IPSTVLSRSD TGSQYIEDSI SQGAVCNKST S--------- ---------- --------
edg4_human   GASTRIMLPE NGHPLMTPPF SYLELQRYAA SNKSTAPDDL WVLLAQPNQQ D-------
edg1_human   AGKFKRPIIA GMEFSRSK.. .SDNSSHPQK DEGDNPETIM SSGNVNSSS- --------
edg3_human   RGARASPIQP ALDPSRSKSS SSNNSSHSPK VKEDLPHTDP SSCIMDKNAA LQNGIFCN
edg5_human   GRRRVGTPGH HLLPLRSSSS LERGMHMPTS PTFLEGNTVV ---------- --------
edg8_human   AAEASGGLRR CLPPGLDGSF SGSERSSPQR DGLDTSGSTG SPGAPTAART LVSEPAAD
edg6_human   AHSGASTTDS SLRP.RDSFR GSRSLSFRMR EPLSSISSVR SI-------- --------
```

FIG. 4

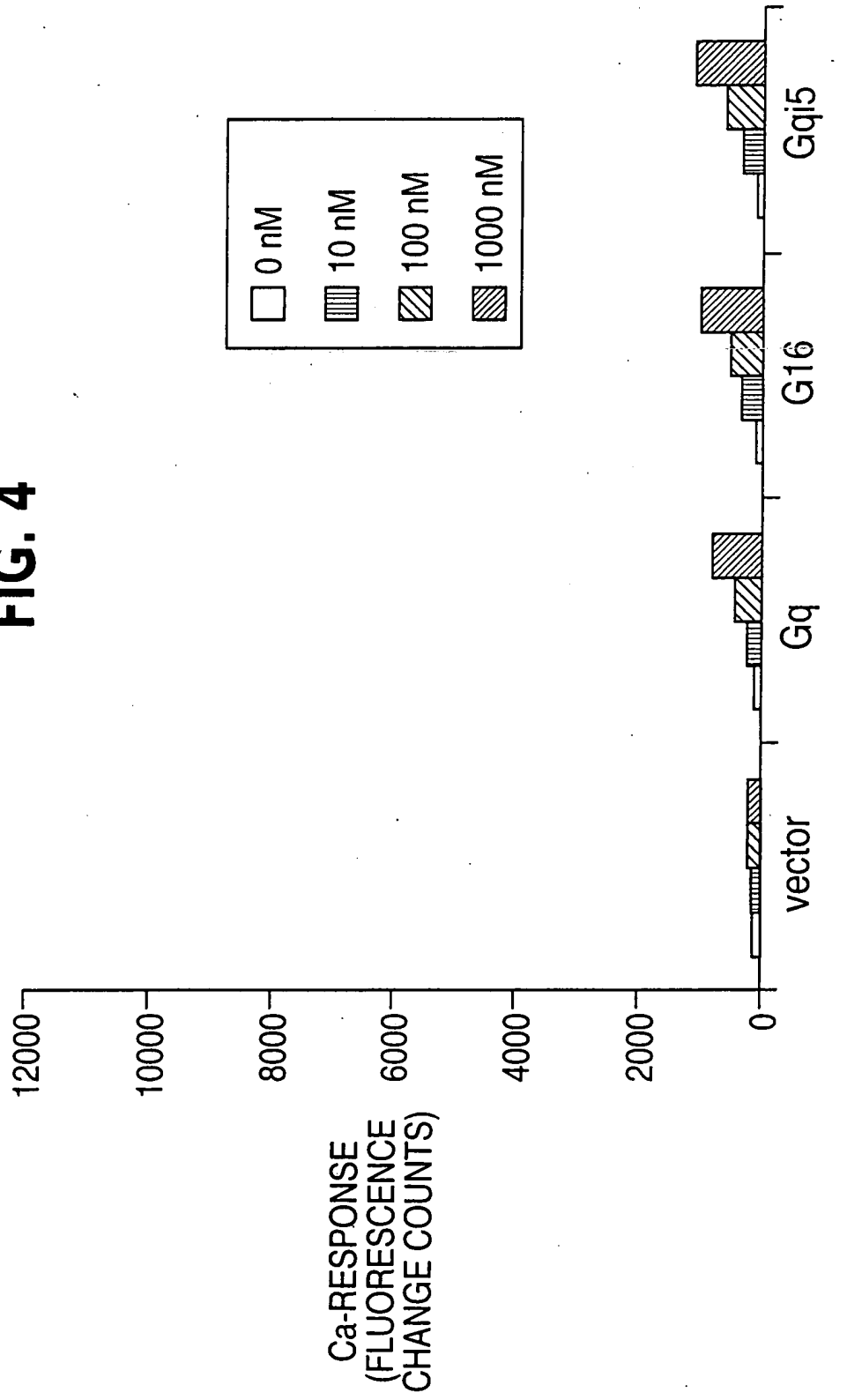


FIG. 5

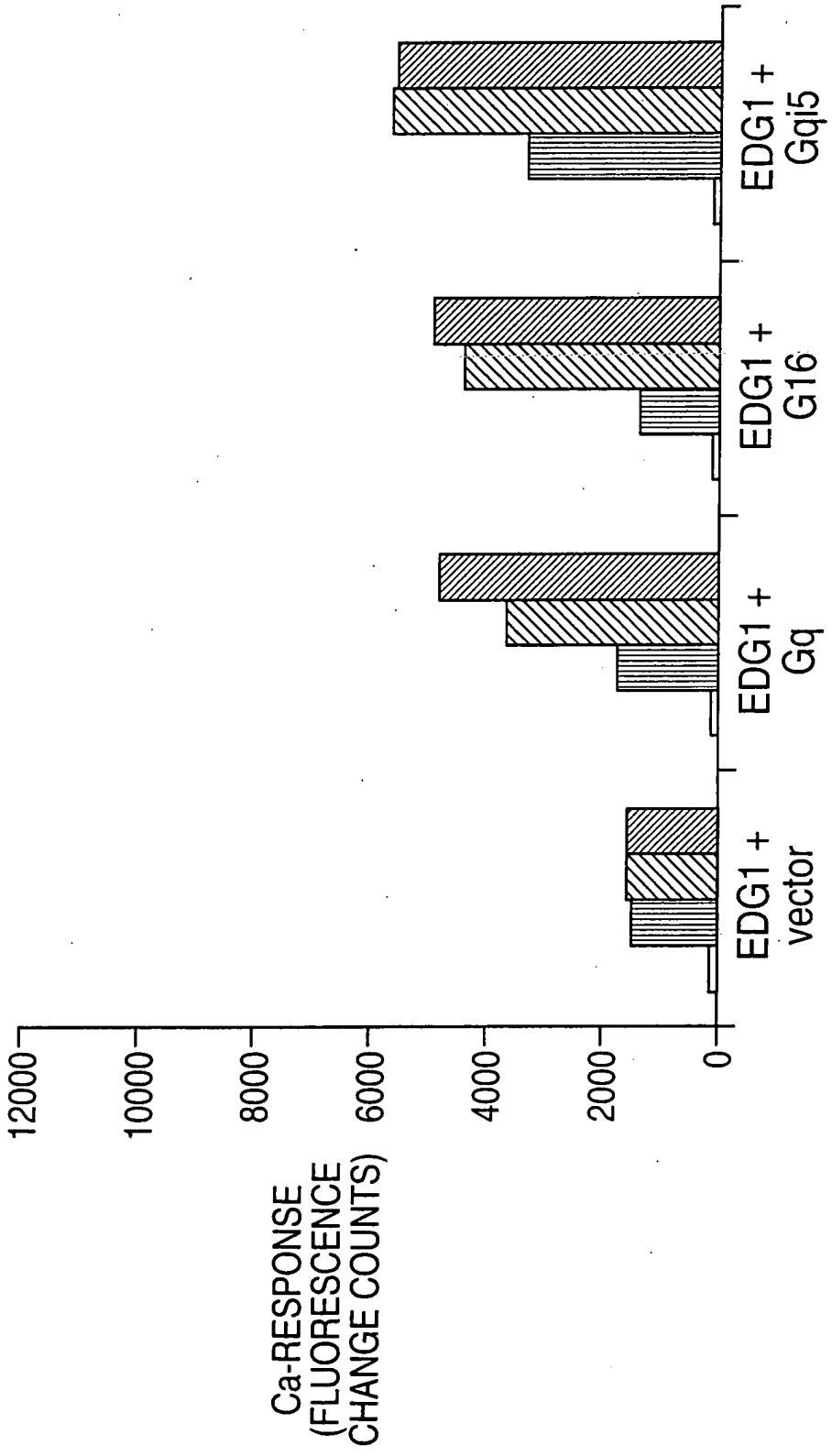


FIG. 6

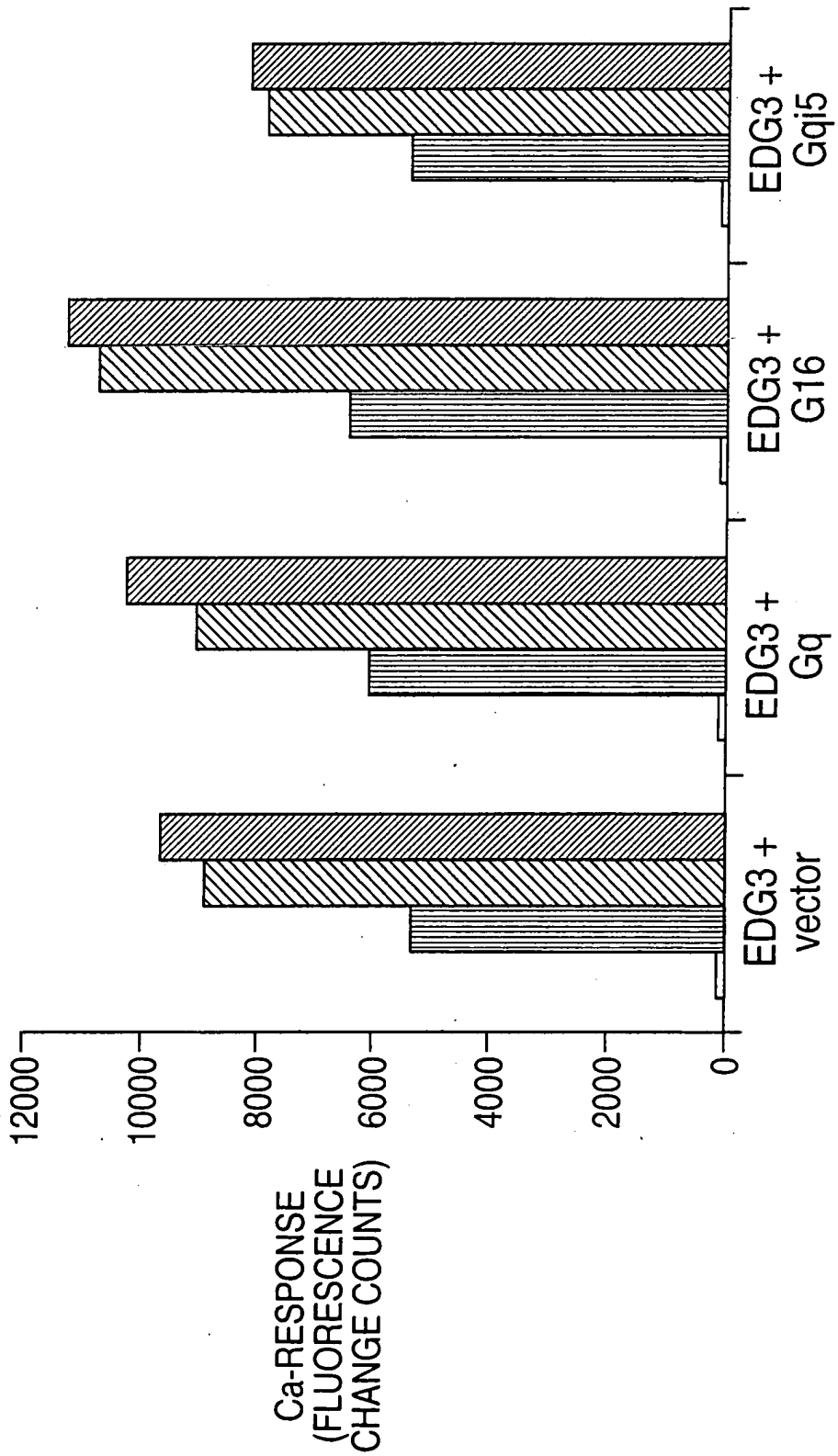


FIG. 7

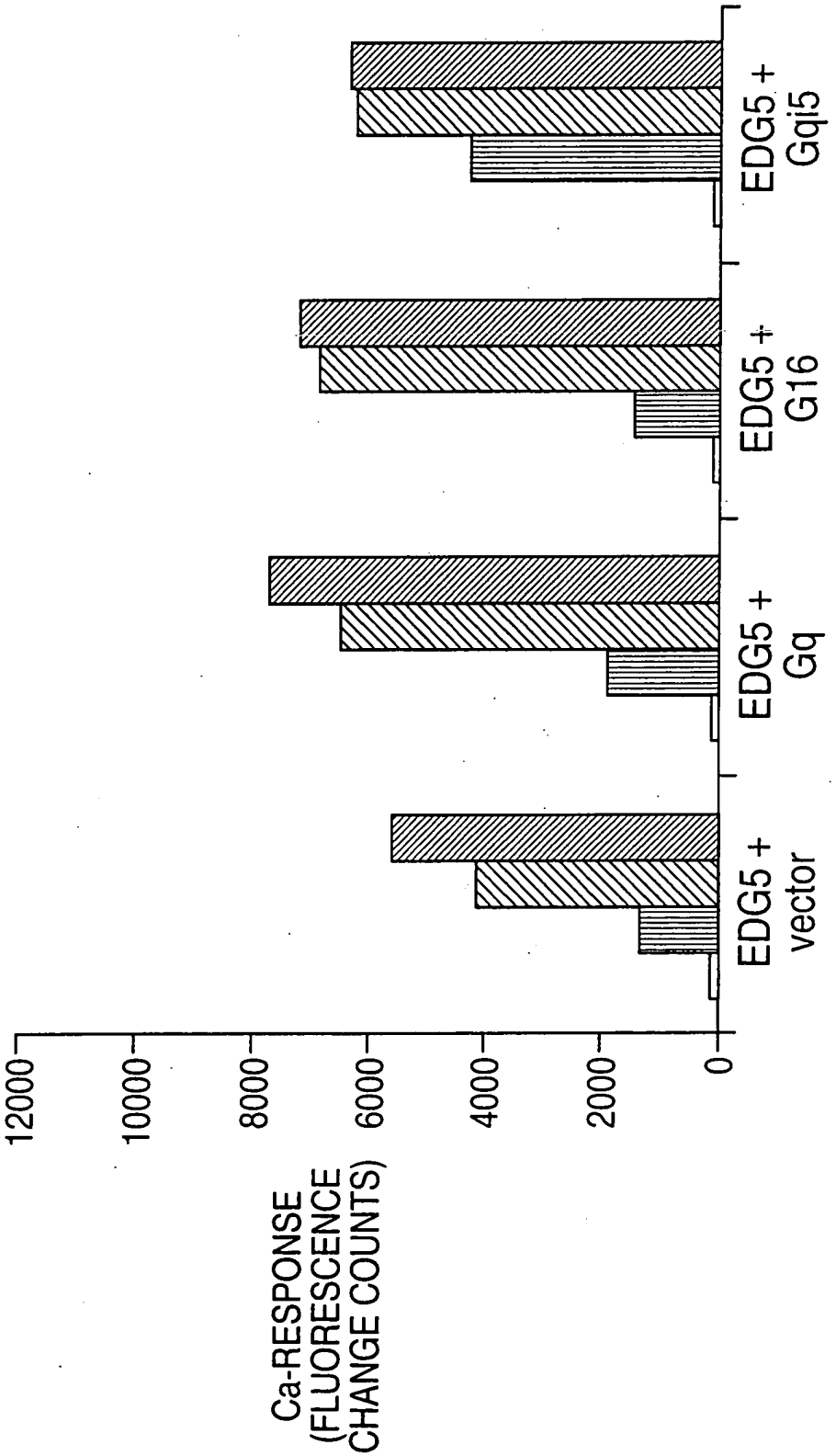


FIG. 8

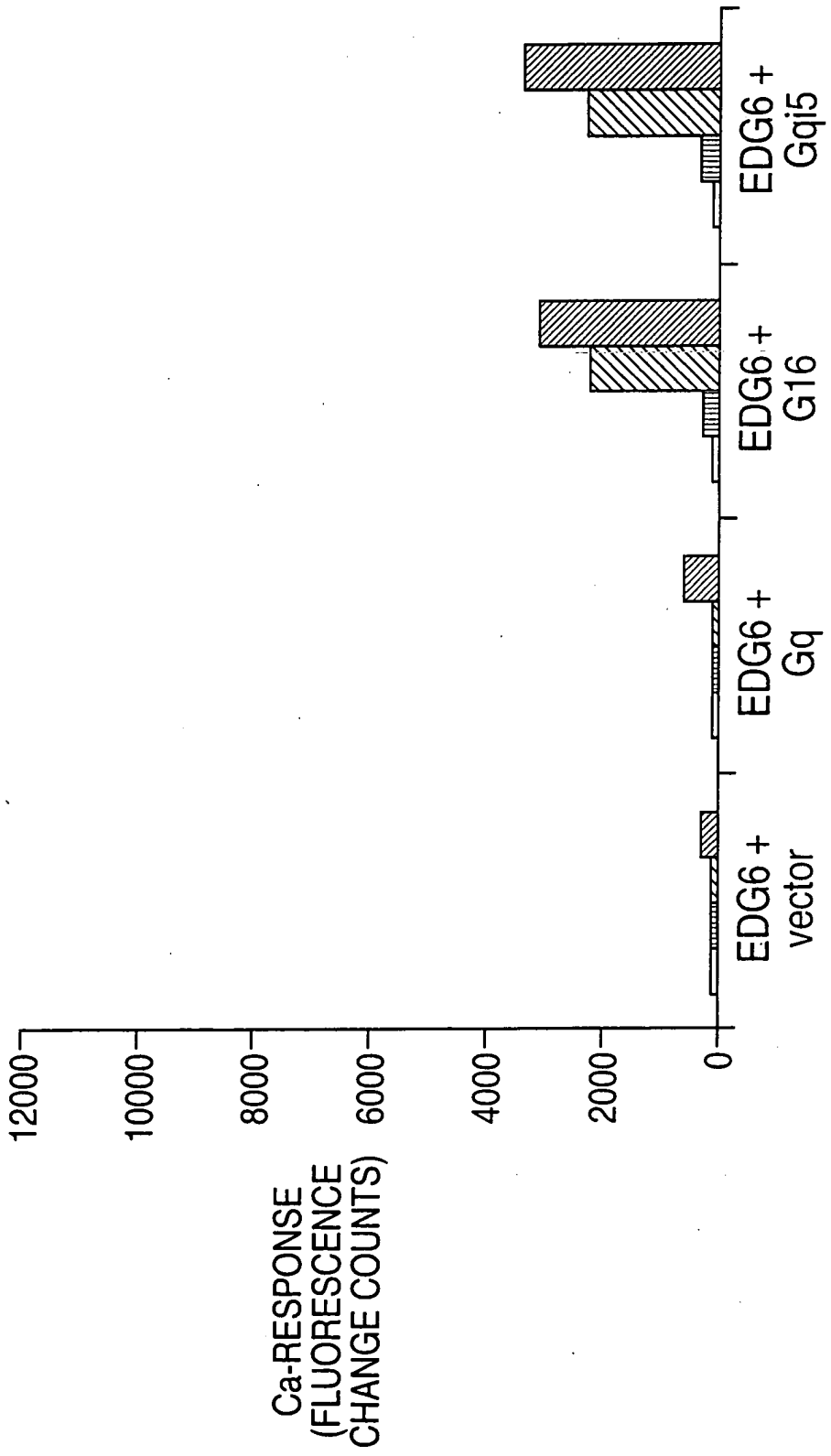


FIG. 9

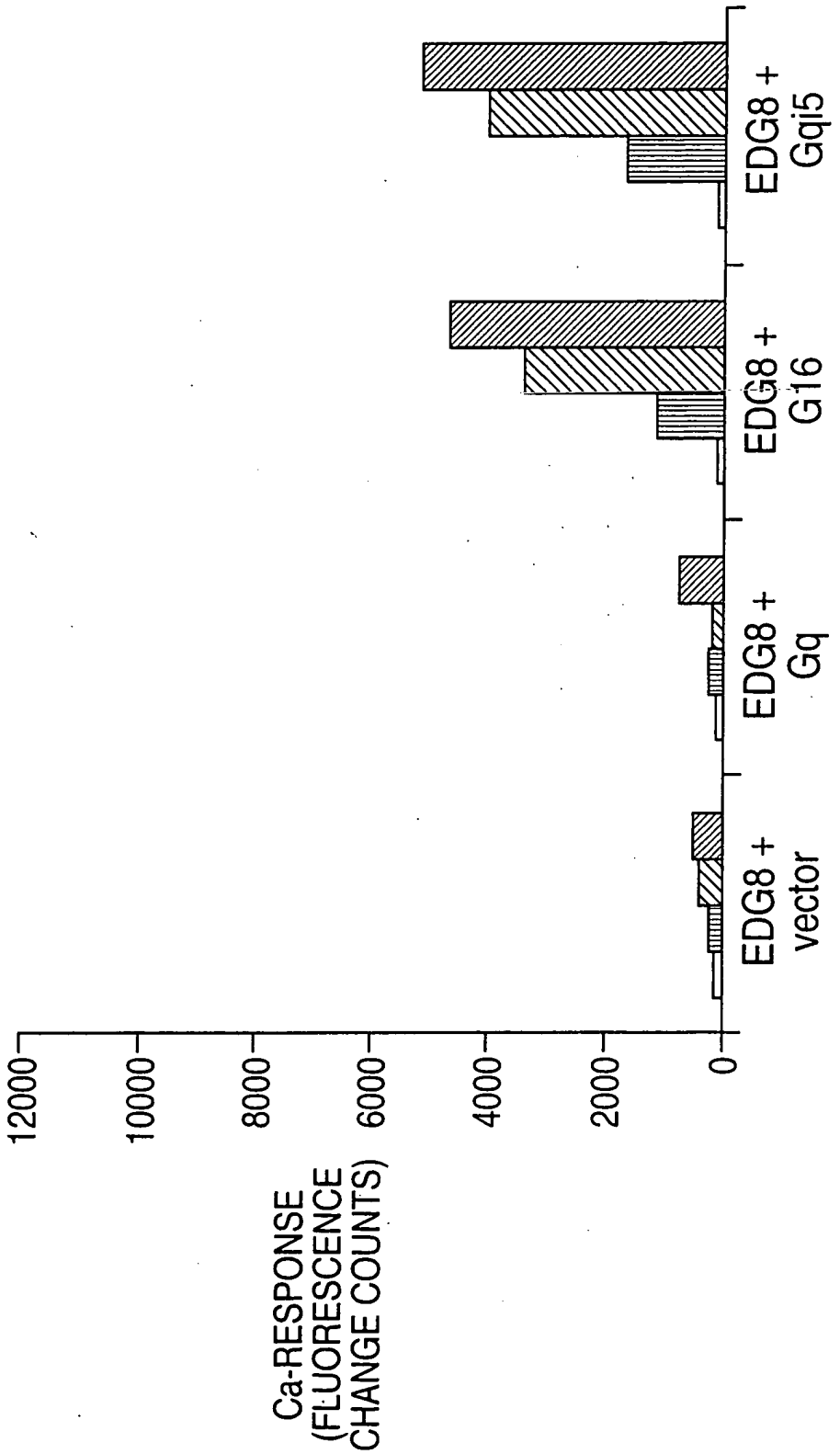


FIG. 10

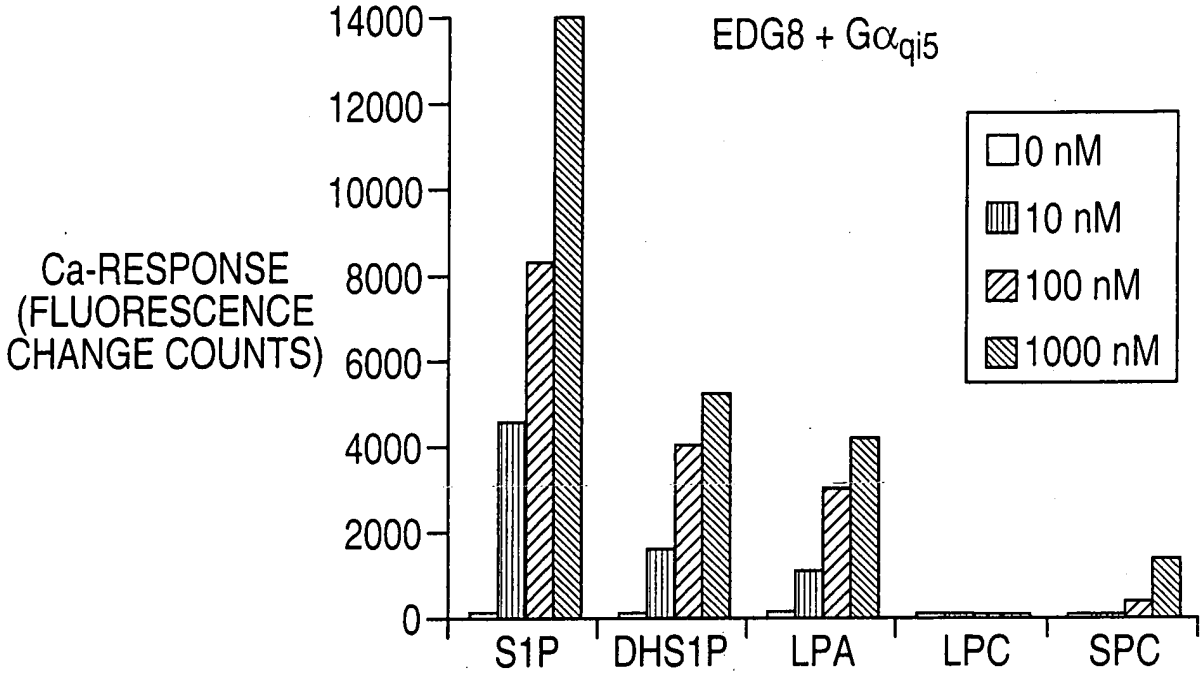


FIG. 11

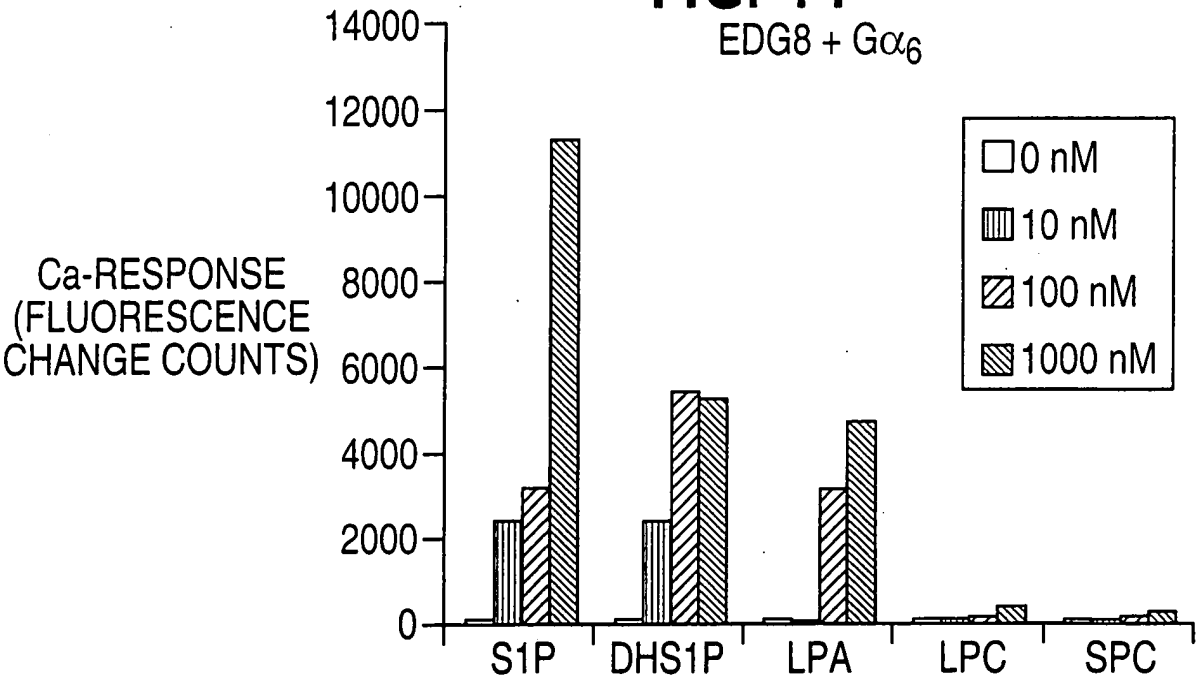


FIG. 12

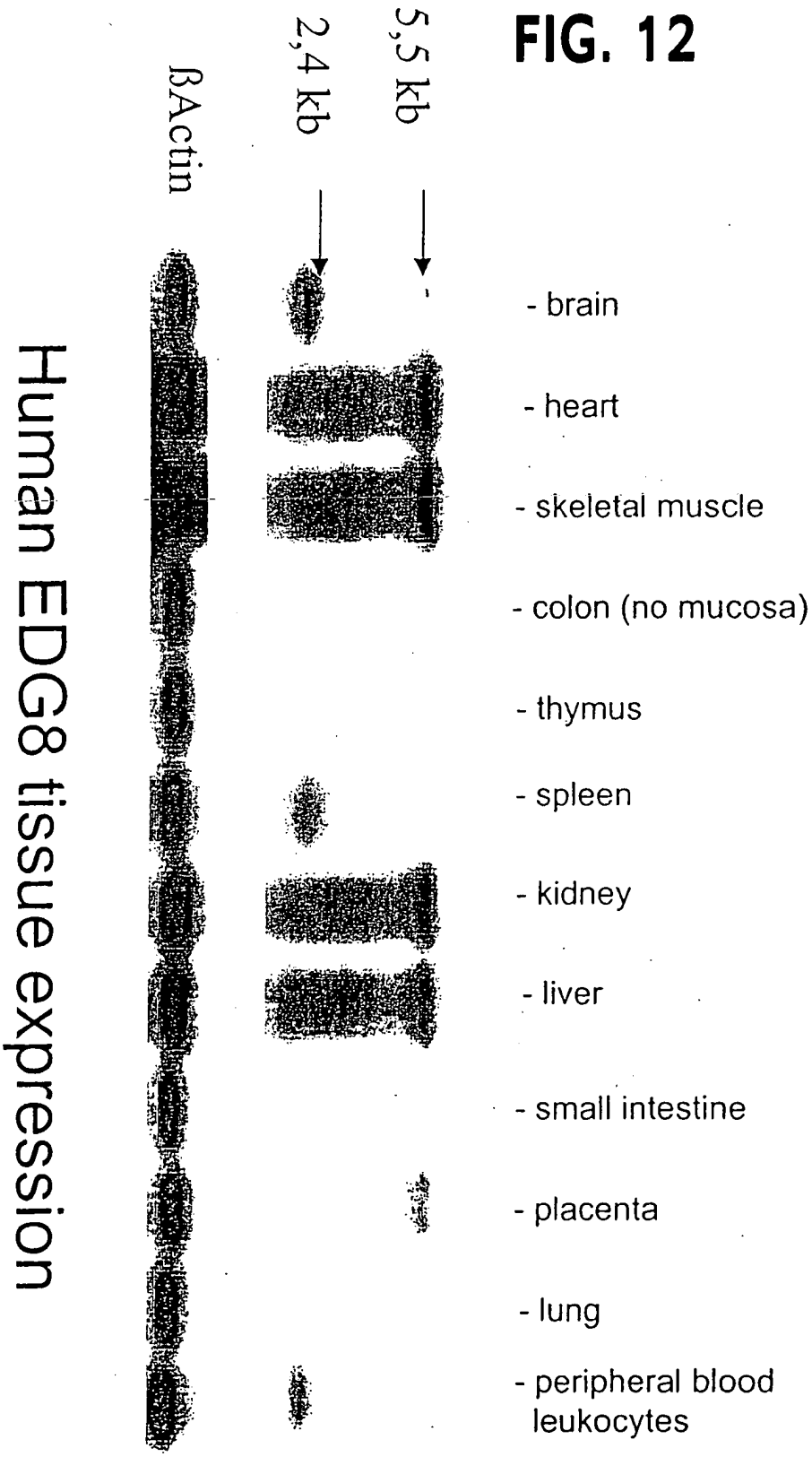


FIG. 13

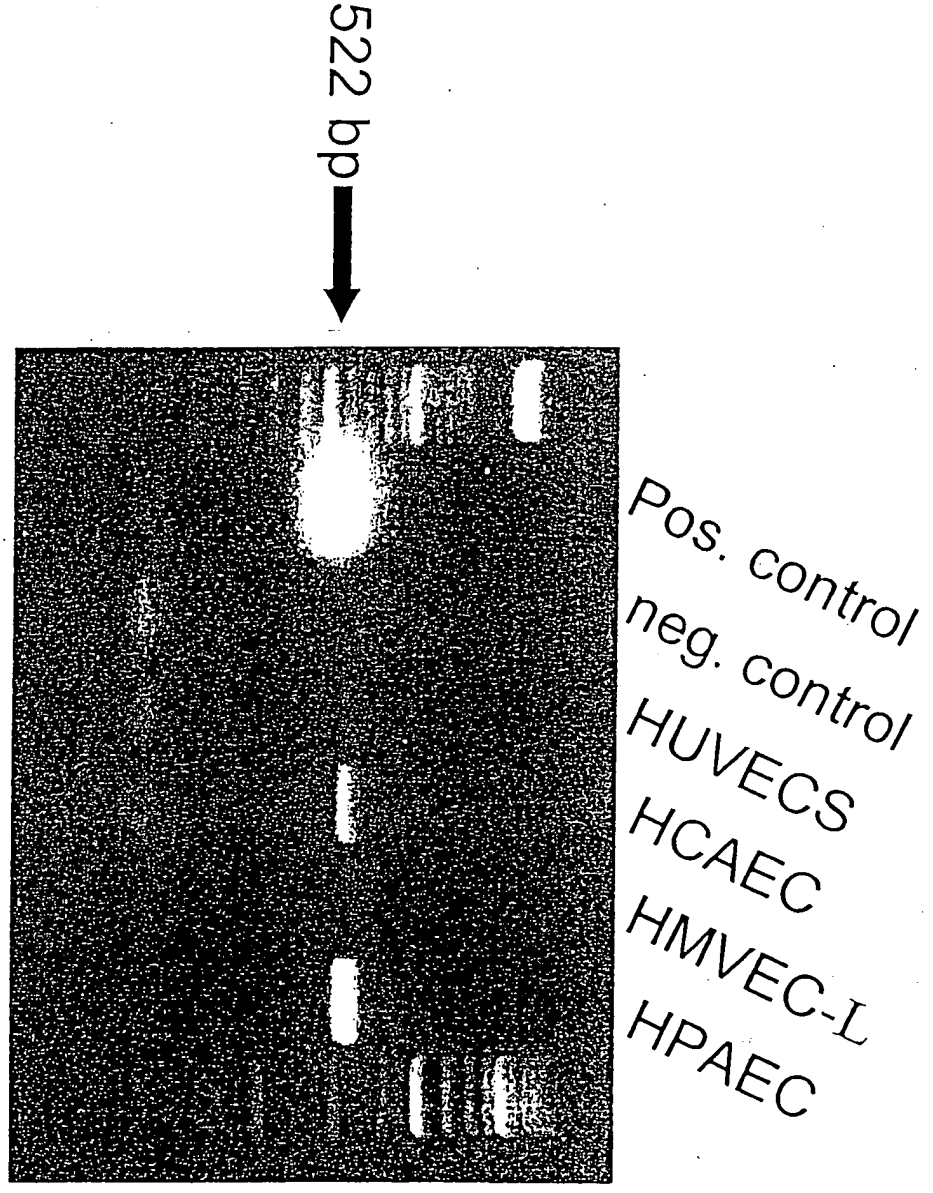


FIG. 14

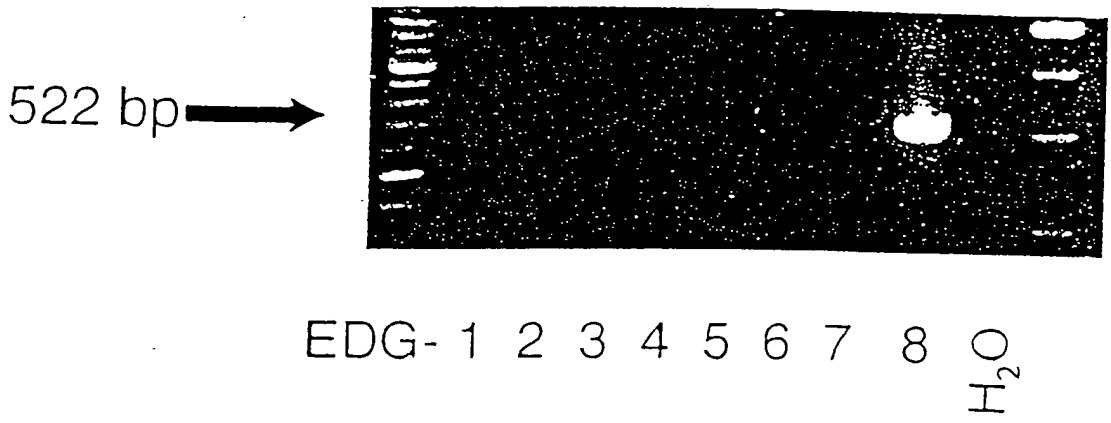


FIG. 15

qi5 background

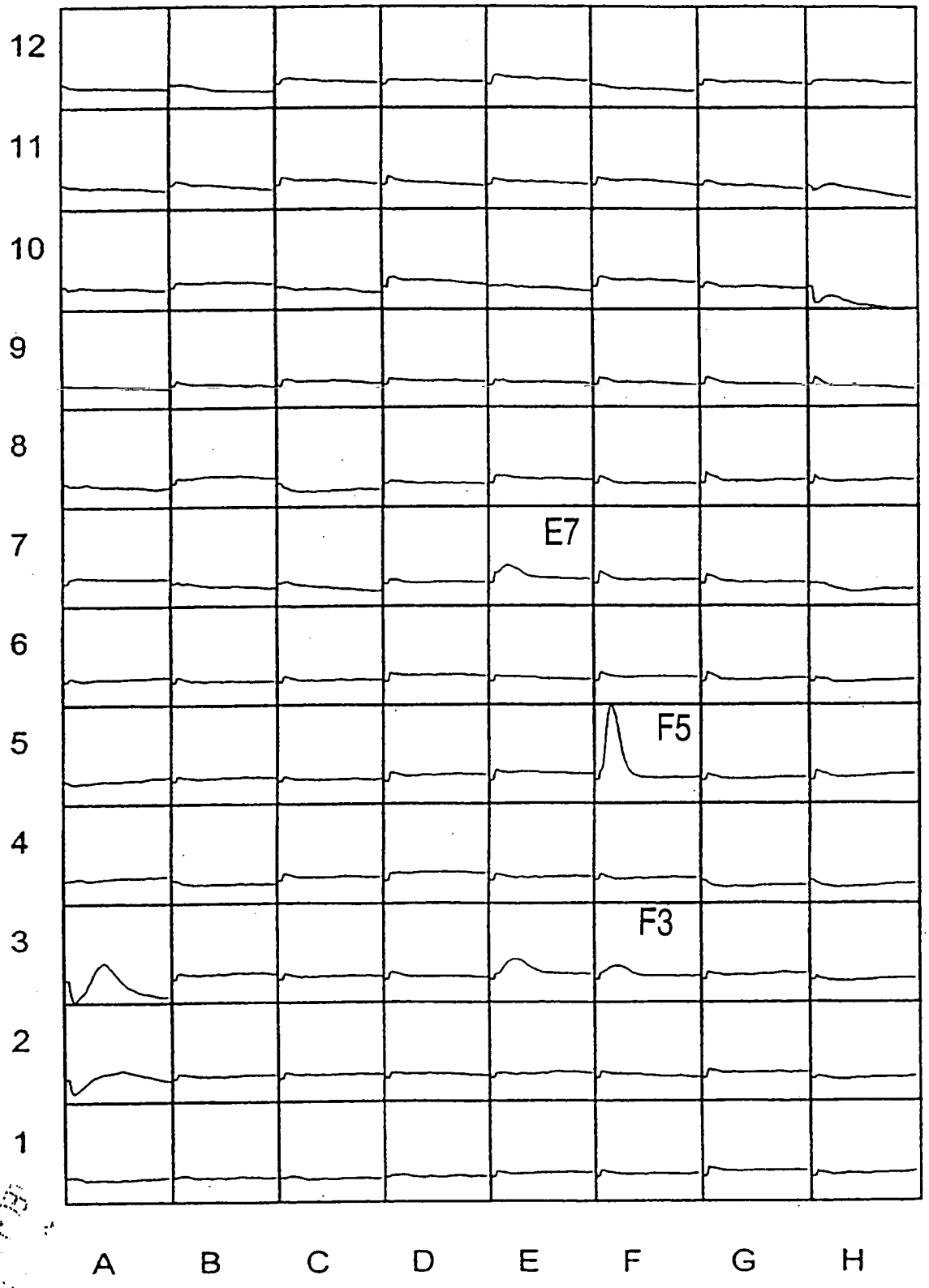


FIG. 16

rEDG8

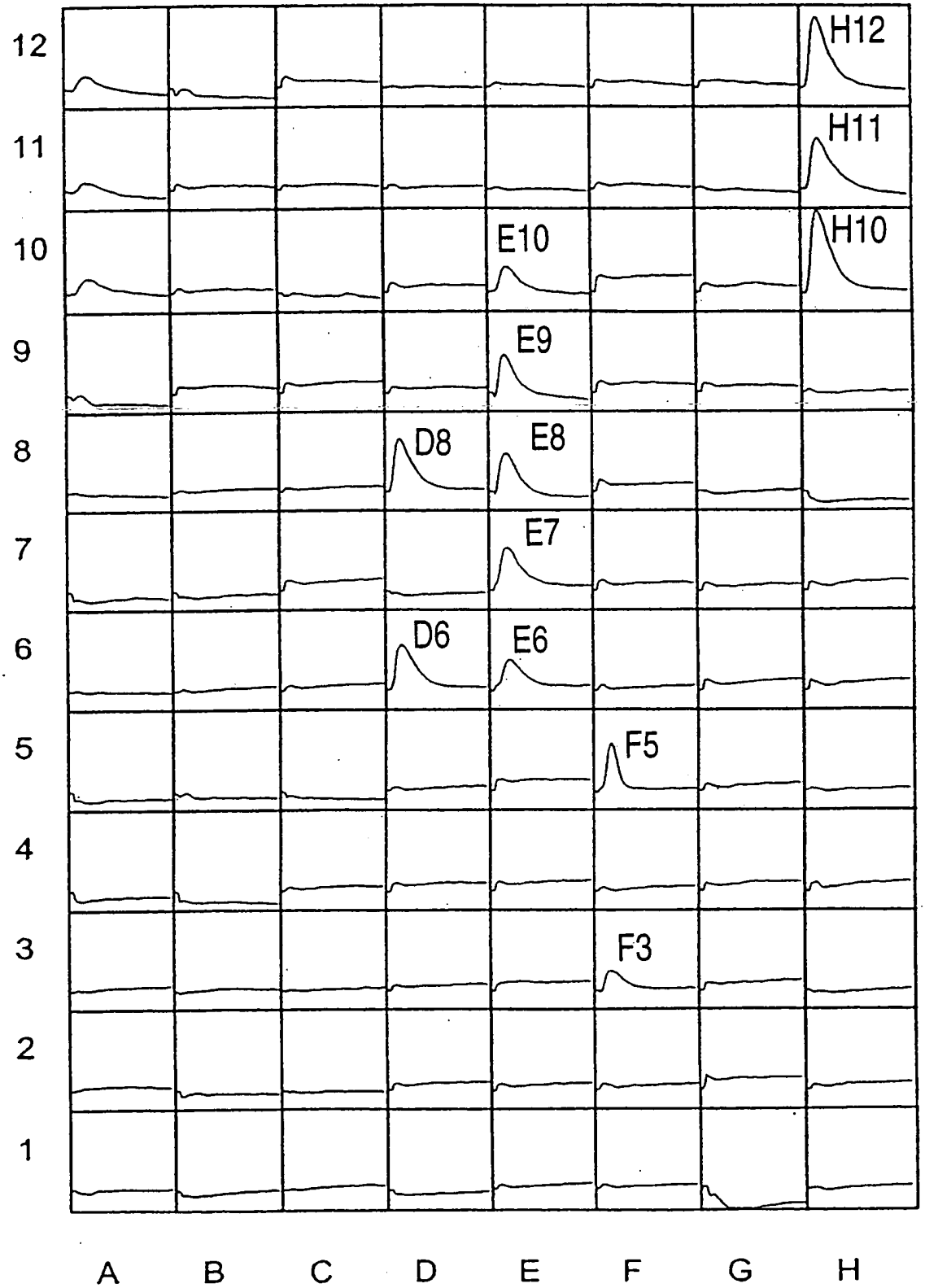


FIG. 17

Fluorescence Change counts

Wells	Lipid	background	rEDG8	stand. response
H10-H12	1μM S1P	0	5196	5196
F5	1μM LPA	5893	4327	-1566
F3	1μM cPAF	1017	1570	553
E10	1μM EPA PAF	0	1354	1354
E9	1μM AA PAF	0	3121	3121
E8	1μM Enantio PAF	0	3883	3883
E7	1μM paf C18:1	1256	3765	2509
E6	1μM Lyso PAF	0	2421	2421
D8	1μM dhS1P	0	5144	5144
D6	1μM S1P	0	3672	3672

FIG. 18

qi5 background in HEK

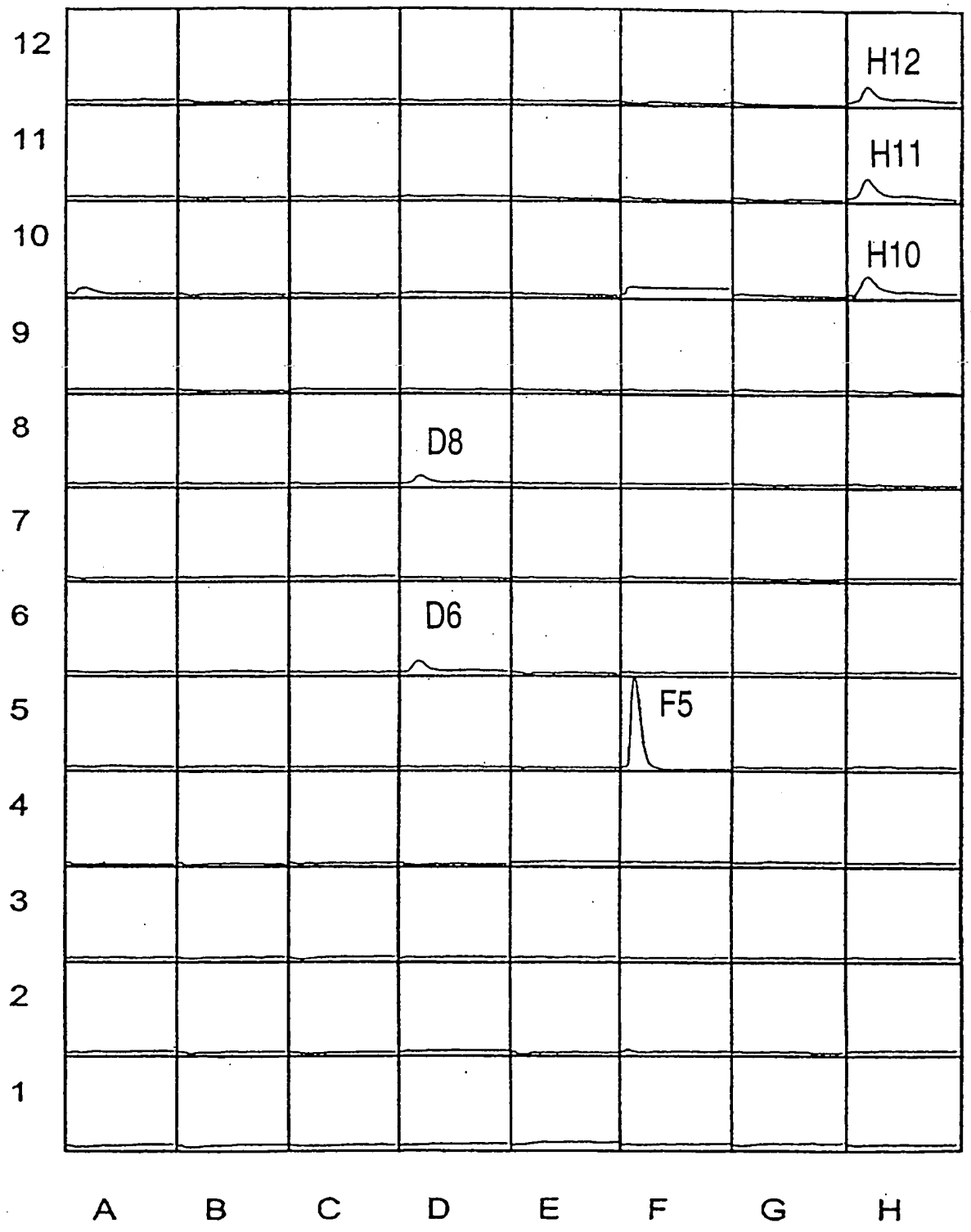


FIG. 19

hEDG8

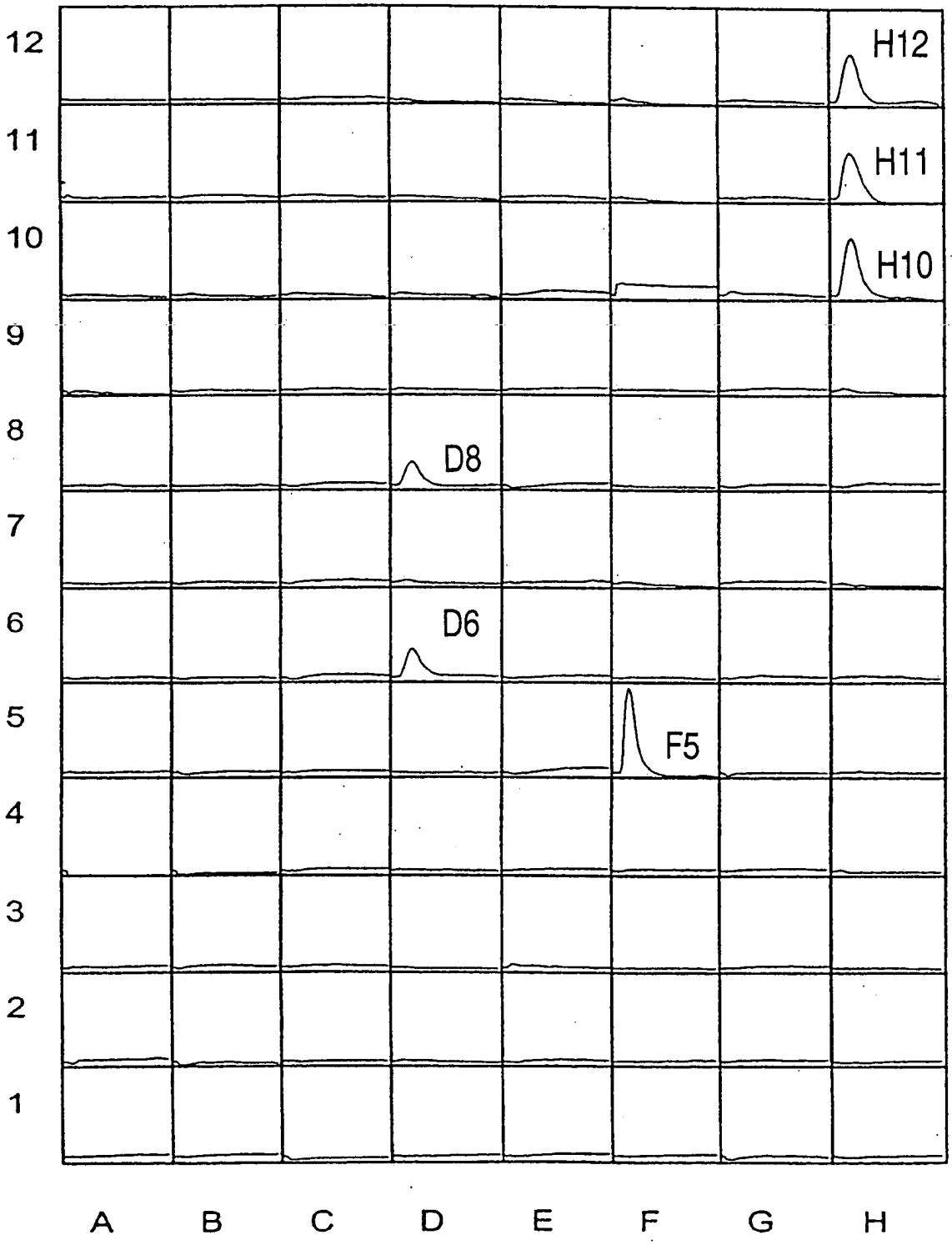
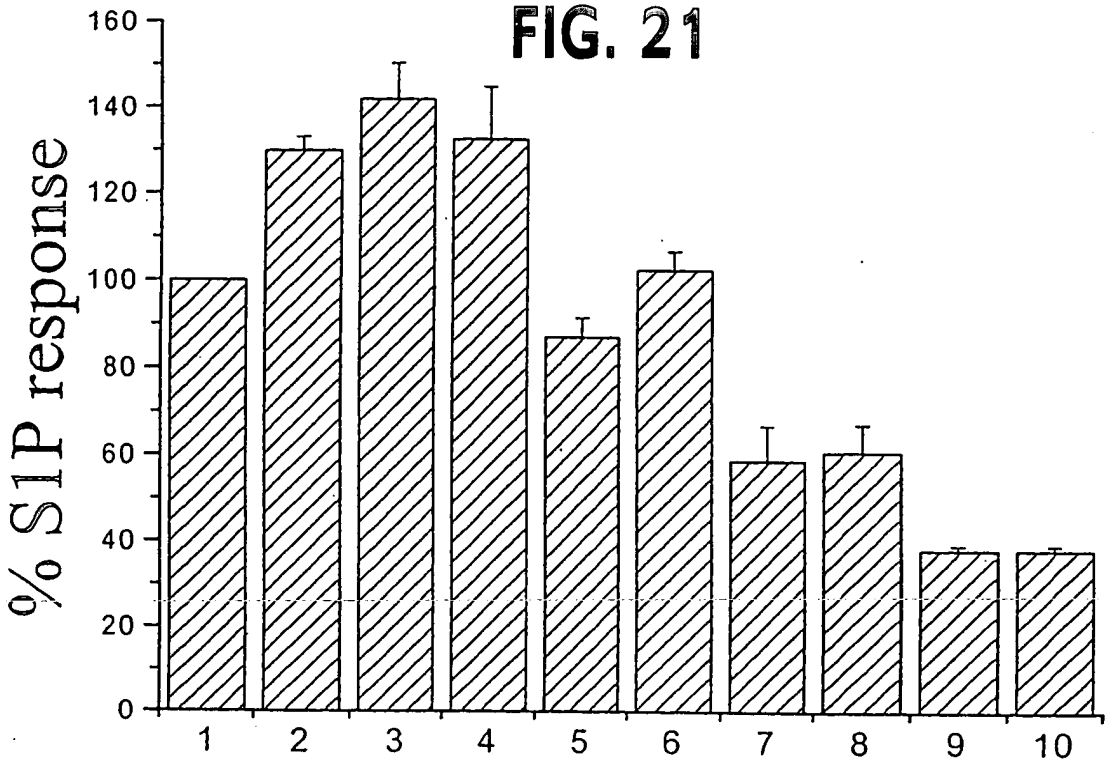


FIG. 20

Fluorescence change counts

Wells	Lipid	background	hEDG8	stand. response
H10-H12	1μM S1P	3696	9493	5797
F5	1μM LPA	18004	16333	-1671
D8	1μM dhS1P	1683	4522	2839
D6	1μM S1P	2273	5605	3332

FIG. 21



1)S1P 2)Leukotrien B4 3)2 DHLA PAF 4)C_2Dihydroceramide
5)15(S)-HEDE 6)PAF C16 7)16,16-Dimethyl PGE_2
8)12(R)-HETE 9)8-Epi-$PGF_{2\alpha}$ 10)Leukotoxin A

FIG. 22

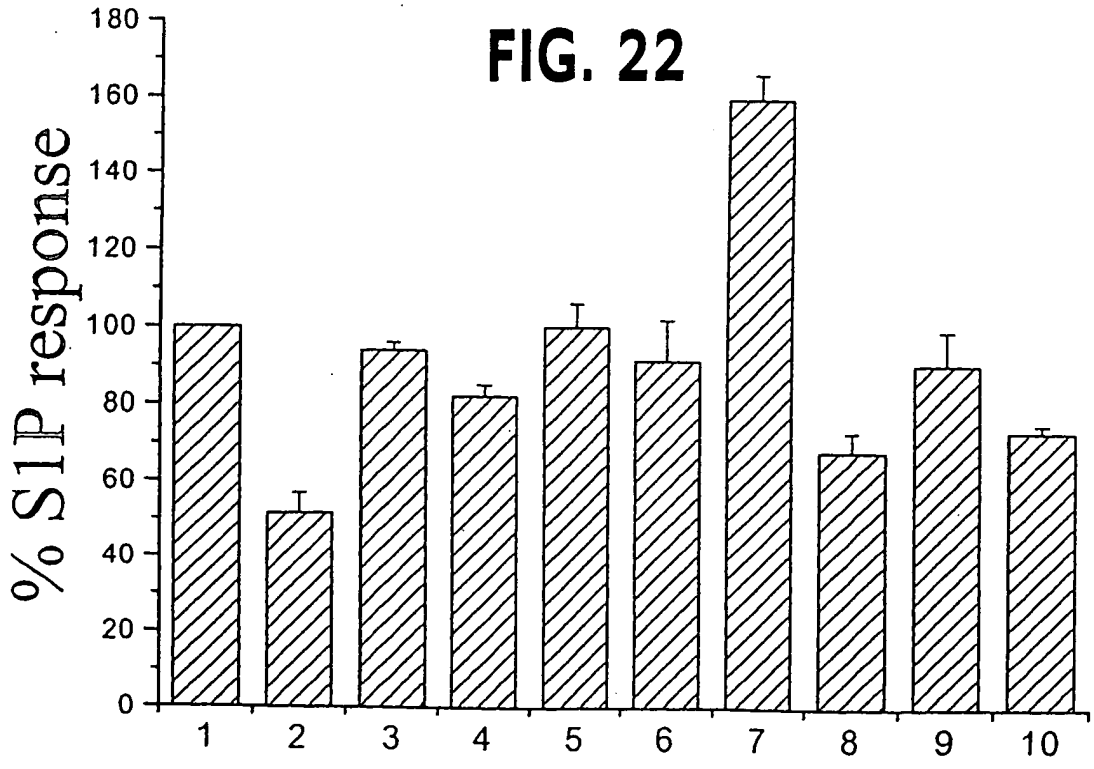


FIG. 23

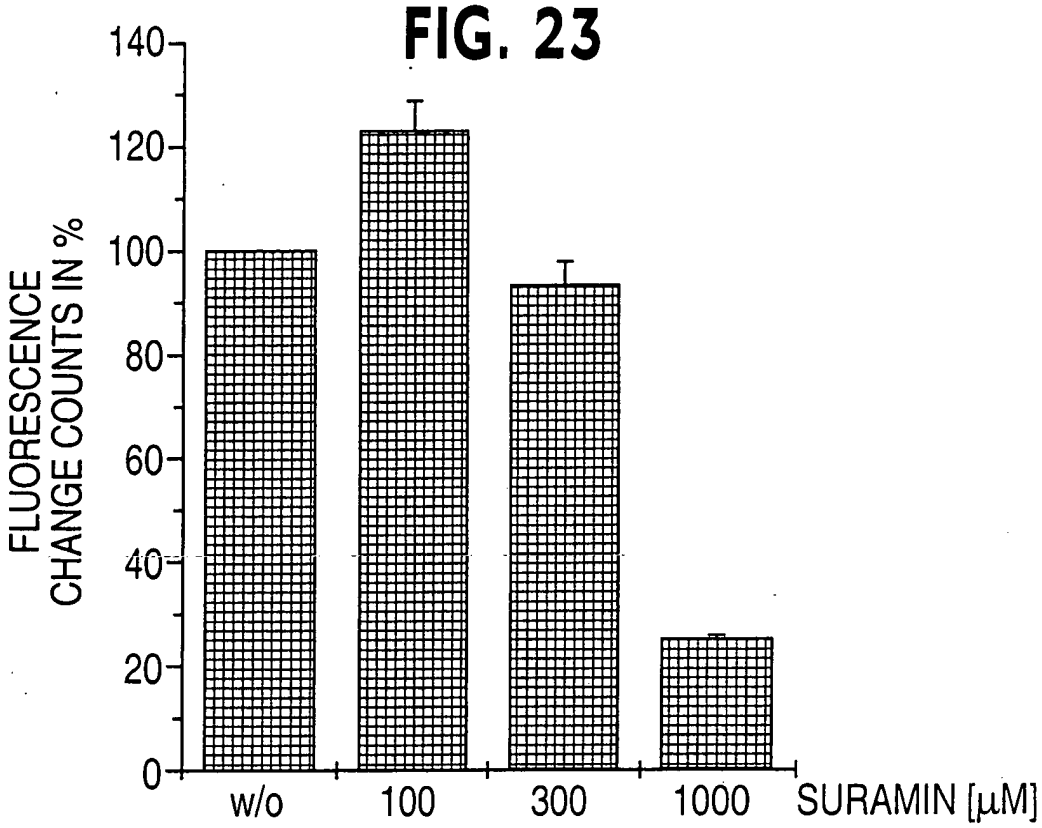


FIG. 24